



BU#11

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/856,617A
Source: PCT09
Date Processed by STIC: 12/4/02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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PCT09

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,617A

DATE: 12/04/2002

TIME: 13:50:11

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Output Set: N:\CRF4\12032002\I856617A.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.,
 5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDE
 7 <130> FILE REFERENCE: 766.52
 9 <140> CURRENT APPLICATION NUMBER: US 09/856,617A
 10 <141> CURRENT FILING DATE: 2001-05-24
 12 <150> PRIOR APPLICATION NUMBER: H10-332484
 13 <151> PRIOR FILING DATE: 1998-11-24
 15 <150> PRIOR APPLICATION NUMBER: H11-248442
 16 <151> PRIOR FILING DATE: 1999-09-02
 18 <160> NUMBER OF SEQ ID NOS: 18
 19 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

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 374 <212> TYPE: DNA
 375 <213> ORGANISM: Mouse
 377 <220> FEATURE:
 378 <221> NAME/KEY: CDS
 379 <222> LOCATION: (107)..(4045)
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 384 tcgggccccg gaacgagccg cgctggcggc ggcggcgcta gccgcg atg atg gag 115
 385 Met Met Glu
 386 1
 388 atc cag atg gac gag gga gga ggt gtg gtg gtg tac caa gac gac tac 163
 389 Ile Gln Met Asp Glu Gly Gly Gly Val Val Val Tyr Gln Asp Asp Tyr
 390 5 10 15
 392 tgc tcg ggc tcg gtc atg tcg gag cgt gtg tcg ggc ctg gcg ggc tcc 211
 393 Cys Ser Gly Ser Val Met Ser Glu Arg Val Ser Gly Leu Ala Gly Ser
 394 20 25 30 35
 396 atc tac cgc gag ttc gag cgc ctc att cac tgc tat gac gag gag gtg 259
 397 Ile Tyr Arg Glu Phe Gly Arg Leu Ile His Cys Tyr Asp Glu Glu Val
 398 40 45 50
 400 gtc aag gag ctc atg ccg ctg gtg gtg aac gtg ctg gag aac ctt gac 307
 401 Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu Asn Leu Asp
 402 55 60 65
 404 tcg gtg ctg agc gag aac cag gag cac gag gtg gag ctg gag ctc cta 355
 405 Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu Glu Leu Leu
 406 70 75 80
 408 cgc gag gac aac gag cag ctg ctc acg caa tac gag cgc gag aag gcg 403

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673 Gly Asn Gly Val Val Ile Ser Ile Pro Leu Thr Glu Thr Val Val Leu
674 1140      1145      1150      1155
676 cat cga ggc cag ctc cta ggg ctc cga gcc aac aag aca tcc cca aca 3619
677 His Arg Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr
678      1160      1165      1170
680 tct ggg gag ggg acc cgc cca ggg ggc atc atc cat gtg tat ggg gac 3667
681 Ser Gly Glu Gly Thr Arg Pro Gly Gly Ile Ile His Val Tyr Gly Asp
682      1175      1180      1185
684 gac agc agt gac aag gcc gcc agt agt ttc atc ccc tac tgc tcc atg 3715
685 Asp Ser Ser Asp Lys Ala Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met
686      1190      1195      1200
688 gca cag gct cag ctt tgc ttc cat ggg cac cgt gat gct gtc aaa ttc 3763
689 Ala Gln Ala Gln Leu Cys Phe His Gly His Arg Asp Ala Val Lys Phe
690      1205      1210      1215
692 ttt gtc tct gtg cca gga aat gtg ctg gcc act ctc aat ggc agt gtg 3811
693 Phe Val Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn Gly Ser Val
694 1220      1225      1230      1235
696 cta gac agc cca tca gag ggc cct ggg cct gct gca ccc gct gca gat 3859
697 Leu Asp Ser Pro Ser Glu Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp
698      1240      1245      1250
700 gct gag ggc cag aag ttg aag aat gca ctg gtg ctg agt ggt ggt gaa 3907
701 Ala Glu Gly Gln Lys Leu Lys Asn Ala Leu Val Leu Ser Gly Gly Glu
702      1255      1260      1265
704 ggt tac att gac ttc cgt atc gga gac gga gag gat gat gaa act gag 3955
705 Gly Tyr Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu
706      1270      1275      1280
708 gaa tgt gcc ggg gac gtg aac cag aca aag ccc tcg ttg tcc aag gct 4003
709 Glu Cys Ala Gly Asp Val Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala
710      1285      1290      1295
E--> 712 gag cgc agc cac atc atc gtg tgg cag gtg tcc tac acc cct gag
713 Glu Arg Ser His Ile Ile Val Trp Gln Val Ser Tyr Thr Pro Glu
714 1300      1305      1310
E--> 716 tgagaccctg tctacactga tgccaactgt acataggacc ctacctgcct gcctccccgc 4102
E--> 718 ctgttccctg gggcagccag gtctgtccat ccccttttaa cctctcaact tgcagctttt 4162
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4043 - counted 4048

RAW SEQUENCE LISTING

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PATENT APPLICATION: US/09/856,617A

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Seq. 8

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2121 gag tct gat ggt gag gat gag cat gag gca ggc cgt gcc ggg cag cca 963
2122 Glu Ser Asp Gly Glu Asp Glu His Glu Ala Gly Arg Ala Gly Gln Pro
2123          305          310          315
2125 gag gct ggt gat ggg acc acc gag atc tca ccc act ggt gct gct ggt 1011
2126 Glu Ala Gly Asp Gly Thr Glu Ile Ser Pro Thr Gly Ala Ala Gly
2127 320          325          330          335
2129 cct gag aag agg atg gag aag aag acg gag cag cag cgg cgg cgg gag 1059
2130 Pro Glu Lys Arg Met Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu
2131          340          345          350
2133 aaa gct gct cgc aag ctg cgg gtg cag cag gct gca ctg agg gca gcc 1107
2134 Lys Ala Ala Arg Lys Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala
2135          355          360          365
2137 cgg ctt cag cac caa gaa ctt ttc agg ctg cgt ggg atc aag gcc cag 1155
2138 Arg Leu Gln His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln
2139          370          375          380
2141 gtg gcc cga agg ctg gca gaa ctg gca cgc cgg agg gag cag cgg cgc 1203
2142 Val Ala Arg Arg Leu Ala Glu Leu Ala Arg Arg Arg Glu Gln Arg Arg
2143          385          390          395
2145 ata cgg cga ctg gca gag gct gac aag ccc cga agg ctg gga cgg ctc 1251
2146 Ile Arg Arg Leu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu
2147 400          405          410          415
2149 aag tac cag gct cct gac att gat gtg cag ctc agc tct gag ttg tct 1299
2150 Lys Tyr Gln Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Ser
2151          420          425          430
2153 ggc tca ctc agg aca ctg aag cca gaa ggt cac att ctc cga gac agg 1347
2154 Gly Ser Leu Arg Thr Leu Lys Pro Glu Gly His Ile Leu Arg Asp Arg
2155          435          440          445
2157 ttc aag agc ttc cag aag aga aat atg att gag ccc cga gaa cga gcc 1395
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2161 aag ttc aag cgc aaa tac aaa gtg aag ctg gtg gag aag cgg gcc tac 1443
2162 Lys Phe Lys Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Tyr
2163          465          470          475
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2166 Arg Glu Ile Gln Leu
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(1469) - counted 1472

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Seq. 9

add. 1/6/01, right margin
so that for d517

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2329 Leu Val Gly Cys Ala Thr Arg Cys Asn Val Pro Arg Ser Asn Cys Ser
2330      820      825      830
2332 Ser Arg Gly Asp Thr Pro Val Leu Asp Lys Gly Gln Gly Asp Val Ala
2333      835      840      845
2335 Thr Thr Ala Asn Gly Lys Val Asn Pro Ser Gln Ser Thr Glu Glu Ala
2336      850      855      860
2338 Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser Glu Ser Glu Ala
2339 865      870      875      880
2341 Thr Thr Val Arg Pro Gly Pro Leu Thr Glu His Val Phe Thr Asp Pro
2342      885      890      895
2344 Ala Pro Thr Pro Ser Ser Ser Thr Gln Pro Ala Ser Glu Asn Gly Ser
2345      900      905      910
2347 Glu Ser Asn Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu
2348      915      920      925
2350 Leu Ser Thr Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala
2351      930      935      940
2353 Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys
2354 945      950      955      960
2356 Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu Ser Leu Val His
2357      965      970      975
2359 Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile
2360      980      985      990
2362 Phe His Arg Gly Glu Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu
2363      995      1000      1005
2365 Met Asp Leu Gly His Pro His Ser Ile Arg Cys Met Ala Val Val
2366      1010      1015      1020
2368 Asn Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln
E--> 2369 1025      1030      1035      1040
2371 Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg
2372      1045      1050      1055
2374 Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val
2375      1060      1065      1070
2377 Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His
2378      1075      1080      1085
2380 Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu
2381      1090      1095      1100
2383 Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu
E--> 2384 1105      1110      1115      1120
2386 Ile Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile
2387      1125      1130      1135
2389 Ser Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu
2390      1140      1145      1150
2392 Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg
2393      1155      1160      1165
2395 Pro Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser Ser Asp Lys Ala
2396      1170      1175      1180
2398 Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys
E--> 2399 1185      1190      1195      1200
2401 Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly

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2405          1220          1225          1230
2407 Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu
2408          1235          1240          1245
2410 Lys Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg
2411          1250          1255          1260
2413 Ile Gly Asp Gly Glu Asp Glu Thr Glu Glu Cys Ala Gly Asp Val
E--> 2414 /265          1270          1275          1280
2416 Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile
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2436 35 40 45
2438 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
2439 50 55 60
2441 Asn Leu Asp Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu
2442 65 70 75 80
2444 Glu Leu Leu Arg Glu Asp Asn Glu Gln Leu Leu Thr Gln Tyr Glu Arg
2445 85 90 95
2447 Glu Lys Ala Leu Arg Lys Gln Ala Glu Glu Lys Phe Ile Glu Phe Glu
2448 100 105 110
2450 Asp Ala Leu Glu Gln Glu Lys Lys Glu Leu Gln Ile Gln Val Glu His
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2453 Tyr Glu Phe Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala
2454 130 135 140
2456 Asp Gln Ile Ser Arg Leu Glu Glu Arg Glu Ser Glu Met Lys Lys Glu
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2459 Tyr Asn Ala Leu His Gln Arg His Thr Glu Met Ile Gln Thr Tyr Val
2460 165 170 175
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2463 180 185 190
2465 Thr Glu Ser Ser Leu Pro Gly Arg Ser Pro Arg Gln Ser Trp Arg Lys
2466 195 200 205
2468 Ser Arg Lys Glu Arg Pro Thr Ser Leu Asn Val Phe Pro Leu Ala Asp
2469 210 215 220
2471 Gly Met Cys Pro Asn Asp Glu Met Ser Glu Ser Gly Gln Ser Ser Ala
2472 225 230 235 240
2474 Ala Ala Thr Pro Ser Thr Thr Gly Thr Lys Ser Asn Thr Pro Thr Ser

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Seq.10

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2628          1060          1065          1070
2630 Ala Trp Ile Gly Asp Gly Val Trp Val Ser Ile Arg Leu Asp Ser Thr
2631          1075          1080          1085
2633 Leu Arg Leu Tyr His Ala His Thr His Gln His Leu Gln Asp Val Asp
2634          1090          1095          1100
2636 Ile Glu Pro Tyr Val Ser Lys Met Leu Gly Thr Gly Lys Leu Gly Phe
E--> 2637 |105          1110          1115          1120
2639 Ser Phe Val Arg Ile Thr Ala Leu Leu Ile Ala Gly Asn Arg Leu Trp
2640          1125          1130          1135
2642 Val Gly Thr Gly Asn Gly Val Val Ile Ser Ile Pro Leu Thr Glu Thr
2643          1140          1145          1150
2645 Val Val Leu His Arg Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr
2646          1155          1160          1165
2648 Ser Pro Thr Ser Gly Glu Gly Thr Arg Pro Gly Gly Ile Ile His Val
2649          1170          1175          1180
2651 Tyr Gly Asp Asp Ser Ser Asp Lys Ala Ala Ser Ser Phe Ile Pro Tyr
E--> 2652 |185          1190          1195          1200
2654 Cys Ser Met Ala Gln Ala Gln Leu Cys Phe His Gly His Arg Asp Ala
2655          1205          1210          1215
2657 Val Lys Phe Phe Val Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn
2658          1220          1225          1230
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2664          1250          1255          1260
2666 Gly Gly Glu Gly Tyr Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp
E--> 2667 |265          1270          1275          1280
2669 Glu Thr Glu Glu Cys Ala Gly Asp Val Asn Gln Thr Lys Pro Ser Leu
2670          1285          1290          1295
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2675 Pro Glu
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2691 Ala Gly Ser Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp
2692 35 40 45
2694 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
2695 50 55 60

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Seq. 11

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2848 865                      870                      875                      880
2850 Thr Thr Ala Asn Gly Lys Val Asn Pro Ser Gln Ser Thr Glu Glu Ala
2851                      885                      890                      895
2853 Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser Glu Ser Glu Ala
2854                      900                      905                      910
2856 Thr Thr Val Arg Pro Gly Pro Leu Thr Glu His Val Phe Thr Asp Pro
2857                      915                      920                      925
2859 Ala Pro Thr Pro Ser Ser Ser Thr Gln Pro Ala Ser Glu Asn Gly Ser
2860 930                      935                      940
2862 Glu Ser Asn Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu
2863 945                      950                      955                      960
2865 Leu Ser Thr Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala
2866                      965                      970                      975
2868 Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys
2869                      980                      985                      990
2871 Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu Ser Leu Val His
2872                      995                      1000                      1005
2874 Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile
2875 1010                      1015                      1020
2877 Phe His Arg Gly Glu Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu
E--> 2878 1025                      1030                      1035                      1040
2880 Met Asp Leu Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val
2881                      1045                      1050                      1055
2883 Asn Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln
2884                      1060                      1065                      1070
2886 Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg
2887 1075                      1080                      1085
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2890 1090                      1095                      1100
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2896                      1125                      1130                      1135
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2899                      1140                      1145                      1150
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2902                      1155                      1160                      1165
2904 Ser Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu
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2911                      1205                      1210                      1215
2913 Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys
2914                      1220                      1225                      1230
2916 Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly

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2917      1235      1240      1245
2919 Asn Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp Ser Pro Ser Glu
2920      1250      1255      1260
2922 Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu
E--> 2923|265      1270      1275      1280
2925 Lys Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg
2926      1285      1290      1295
2928 Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val
2929      1300      1305      1310
2931 Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile
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2950 Ala Gly Ser Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp
2951      35      40      45
2953 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
2954      50      55      60
2956 Asn Leu Asp Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu
2957 65      70      75      80
2959 Glu Leu Leu Arg Glu Asp Asn Glu Gln Leu Leu Thr Gln Tyr Glu Arg
2960      85      90      95
2962 Glu Lys Ala Leu Arg Lys Gln Ala Glu Glu Lys Phe Ile Glu Phe Glu
2963      100      105      110
2965 Asp Ala Leu Glu Gln Glu Lys Lys Glu Leu Gln Ile Gln Val Glu His
2966      115      120      125
2968 Tyr Glu Phe Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala
2969      130      135      140
2971 Asp Gln Ile Ser Arg Leu Glu Glu Arg Glu Ser Glu Met Lys Lys Glu
2972 145      150      155      160
2974 Tyr Asn Ala Leu His Gln Arg His Thr Glu Met Ile Gln Thr Tyr Val
2975      165      170      175
2977 Glu His Ile Glu Arg Ser Lys Met Gln Gln Val Gly Gly Ser Gly Gln
2978      180      185      190
2980 Thr Glu Ser Ser Leu Pro Gly Arg Lys Glu Arg Pro Thr Ser Leu
2981      195      200      205
2983 Asn Val Phe Pro Leu Ala Asp Gly Met Val Arg Ala Gln Met Gly Gly
2984      210      215      220
2986 Lys Leu Val Pro Ala Gly Asp His Trp His Leu Ser Asp Leu Gly Gln
2987 225      230      235      240
2989 Leu Gln Ser Ser Ser Ser Tyr Gln Cys Pro Asn Asp Glu Met Ser Glu

```

RAW SEQUENCE LISTING

DATE: 12/04/2002

PATENT APPLICATION: US/09/856,617A

TIME: 13:50:11

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12032002\I856617A.raw

seq. 12

```

E--> 3137|025          1030          1035          1040
3139 Asp Leu Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val Asn
3140          1045          1050          1055
3142 Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln Pro
3143          1060          1065          1070
3145 Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg Glu
3146          1075          1080          1085
3148 Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val Ser
3149          1090          1095          1100
3151 Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His Gln
E--> 3152|105          1110          1115          1120
3154 His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu Gly
3155          1125          1130          1135
3157 Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu Ile
3158          1140          1145          1150
3160 Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile Ser
3161          1155          1160          1165
3163 Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu Gly
3164          1170          1175          1180
3166 Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg Pro
E--> 3167|185          1190          1195          1200
3169 Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser Ser Asp Lys Ala Ala
3170          1205          1210          1215
3172 Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys Phe
3173          1220          1225          1230
3175 His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly Asn
3176          1235          1240          1245
3178 Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp Ser Pro Ser Glu Gly
3179          1250          1255          1260
3181 Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu Lys
E--> 3182|265          1270          1275          1280
3184 Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg Ile
3185          1285          1290          1295
3187 Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val Asn
3188          1300          1305          1310
3190 Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile Val
3191          1315          1320          1325
3193 Trp Gln Val Ser Tyr Thr Pro Glu
3194          1330          1335
3285 <210> SEQ ID NO: 14
3286 <211> LENGTH: 1508
3287 <212> TYPE: PRT
3288 <213> ORGANISM: Mouse
3290 <400> SEQUENCE: 14
3291 Met Met Ala Gly Glu Gly Ser Thr Ile Thr Ser Arg Ile Lys Asn Leu
3292 1 5 10 15
3294 Leu Arg Ser Pro Ser Ile Lys Leu Arg Arg Ser Lys Ala Gly Asn Arg
3295 20 25 30
3297 Arg Glu Asp Leu Ser Ser Lys Val Thr Leu Glu Lys Val Leu Gly Val

```

RAW SEQUENCE LISTING

DATE: 12/04/2002

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TIME: 13:50:11

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12032002\I856617A.raw

Seq. 14

```

3445          820          825          830
3447 Met Ser Arg Ala Gln Glu Thr Met Glu Tyr Leu Asp Pro Ala Pro Val
3448          835          840          845
3450 Ala Asn Thr Gly Pro Lys Arg Arg Gly Arg Trp Ala Gln Pro Gly Val
3451          850          855          860
3453 Glu Leu Ser Val Arg Ser Met Leu Asp Leu Arg Gln Ile Glu Thr Leu
3454 865          870          875          880
3456 Ala Pro Ser Pro Arg Gly Pro Ser Gln Asp Ser Leu Ala Val Ser Pro
3457          885          890          895
3459 Ala Gly Pro Gly Lys His Gly Pro Gln Ala Pro Glu Leu Ser Cys Val
3460          900          905          910
3462 Ser Gln Asn Glu Arg Ala Pro Arg Leu Gln Thr Ser Gln Pro Cys Ser
3463          915          920          925
3465 Cys Pro Asp Ile Ile Gln Leu Leu Ser Gln Glu Glu Gly Val Phe Ala
3466          930          935          940
3468 Gln Asp Leu Glu Pro Ala Pro Ile Glu Asp Gly Ile Val Tyr Pro Glu
3469 945          950          955          960
3471 Pro Ser Asp Ser Pro Thr Met Asp Thr Ser Ala Phe Gln Val Gln Ala
3472          965          970          975
3474 Pro Thr Gly Gly Ser Leu Gly Arg Met Tyr Pro Gly Ser Arg Gly Ser
3475          980          985          990
3477 Glu Lys His Ser Pro Asp Ser Ala Cys Ser Val Asp Tyr Ser Ser Ser
3478          995          1000          1005
3480 Arg Leu Ser Ser Pro Glu His Pro Asn Glu Asp Ser Glu Ser Thr Glu
3481 1010          1015          1020
3483 Pro Leu Ser Val Asp Gly Ile Ser Ser Asp Leu Glu Glu Pro Ala Glu
E--> 3484 1025          1030          1035          1040
3486 Gly Asp Glu Asp Glu Glu Glu Gly Gly Thr Gly Leu Cys Gly Leu
3487          1045          1050          1055
3489 Gln Glu Gly Gly Pro Arg Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln
3490          1060          1065          1070
3492 Leu Phe Glu Thr Leu Ala Asn Gly Thr Ala Pro Gly Gly Pro Ala Arg
3493          1075          1080          1085
3495 Val Leu Glu Arg Thr Glu Ser Arg Ser Ile Ser Ser Arg Phe Leu Leu
3496          1090          1095          1100
3498 Gln Val Gln Thr Leu Pro Leu Arg Glu Pro Ser Leu Ser Ser Ser Gly
E--> 3499 1105          1110          1115          1120
3501 Leu Ala Leu Thr Ser Arg Pro Asp Gln Val Ser Gln Val Ser Gly Glu
3502          1125          1130          1135
3504 Gln Leu Lys Gly Ser Gly Ala Thr Pro Pro Gly Ala Pro Pro Glu Met
3505          1140          1145          1150
3507 Glu Pro Ser Ser Gly Asn Ser Gly Pro Lys Gln Val Ala Pro Val Leu
3508          1155          1160          1165
3510 Leu Thr Arg Arg Arg Asn Asn Leu Asp Asn Ser Trp Ala Ser Lys Lys
3511          1170          1175          1180
3513 Met Ala Ala Thr Arg Pro Leu Ala Gly Leu Gln Lys Ala Gln Ser Val
E--> 3514 1185          1190          1195          1200
3516 His Ser Leu Val Pro Gln Asp Glu Val Pro Ser Ser Arg Pro Leu Leu
3517          1205          1210          1215

```

RAW SEQUENCE LISTING

DATE: 12/04/2002

PATENT APPLICATION: US/09/856,617A

TIME: 13:50:11

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12032002\I856617A.raw

```

3519 Phe Arg Glu Ala Glu Thr Gln Gly Ser Leu Gly Ser Leu Pro Gln Ala
3520           1220           1225           1230
3522 Gly Gly Cys Ser Ser Gln Pro His Ser Tyr Gln Asn His Thr Thr Ser
3523           1235           1240           1245
3525 Ser Met Ala Lys Leu Ala Arg Ser Ile Ser Val Gly Glu Asn Pro Gly
3526           1250           1255           1260
3528 Leu Ala Thr Glu Pro Gln Ala Pro Ala Pro Ile Arg Ile Ser Pro Phe
E--> 3529 | 265           1270           1275           1280
3531 Asn Lys Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp Ile Pro
3532           1285           1290           1295
3534 Lys Pro Leu Pro Asp Arg Pro Thr Leu Thr Thr Phe Ser Pro Val Ser
3535           1300           1305           1310
3537 Lys Gly Leu Thr His Asn Glu Thr Glu Gln Ser Gly Pro Leu Arg Glu
3538           1315           1320           1325
3540 Pro Arg Lys Ala His Thr Thr Val Glu Lys His Ser Cys Leu Gly Glu
3541           1330           1335           1340
3543 Gly Thr Thr His Lys Ser Arg Thr Glu Cys Gln Ala Tyr Pro Gly Pro
E--> 3544 | 345           1350           1355           1360
3546 Asn His Pro Cys Arg Gln Gln Leu Pro Val Asn Asn Leu Leu Gln Ala
3547           1365           1370           1375
3549 Glu Ser Leu Gln Pro Leu Ser Pro Glu Lys Thr Arg Asn Pro Val Glu
3550           1380           1385           1390
3552 Ser Ser Arg Pro Gly Val Ala Leu Ser Gln Asp Ser Glu Leu Ala Leu
3553           1395           1400           1405
3555 Ser Leu Gln Gln Cys Glu Gln Leu Val Ala Glu Leu Gln Gly Asn Val
3556           1410           1415           1420
3558 Arg Gln Ala Val Glu Leu Tyr Arg Ala Val Thr Ser Cys Lys Thr Pro
E--> 3559 | 425           1430           1435           1440
3561 Ser Ala Glu Gln Ser His Ile Thr Arg Leu Leu Arg Asp Thr Phe Ser
3562           1445           1450           1455
3564 Pro Val Arg Gln Glu Leu Glu Val Leu Ala Gly Ala Val Leu Ser Ser
3565           1460           1465           1470
3567 Pro Gly Gly Ser Pro Gly Ala Val Ala Ala Glu Gln Thr Gln Ala Leu
3568           1475           1480           1485
3570 Leu Glu Gln Tyr Ser Glu Leu Leu Leu Arg Ala Val Glu Arg Arg Met
3571           1490           1495           1500
3573 Glu Arg Arg Leu
E--> 3574 | 505
3730 <210> SEQ ID NO: 17
3731 <211> LENGTH: 27
3732 <212> TYPE: DNA
3733 <213> ORGANISM: Artificial Sequence
3735 <220> FEATURE:
3736 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
3738 <400> SEQUENCE: 17
E--> 3739 tagatatcgc cttggaacaa gagaaga
3740 (27) -----> place here
3743 <210> SEQ ID NO: 18
3744 <211> LENGTH: 31

```

RAW SEQUENCE LISTING

DATE: 12/04/2002

PATENT APPLICATION: US/09/856,617A

TIME: 13:50:11

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12032002\I856617A.raw

3745 <212> TYPE: DNA

3746 <213> ORGANISM: Artificial Sequence

3748 <220> FEATURE:

3749 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

3751 <400> SEQUENCE: 18

3752 atgaattctc agttgttctt tgtgacactg a

31

E--> 3753 1 / 142 - delete

VERIFICATION SUMMARY

DATE: 12/04/2002

PATENT APPLICATION: US/09/856,617A

TIME: 13:50:12

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12032002\I856617A.raw

L:712 M:254 E: No. of Bases conflict, LENGTH:Input:4043 Counted:4048 SEQ:2
M:254 Repeated in SeqNo=2
L:2165 M:254 E: No. of Bases conflict, LENGTH:Input:1469 Counted:1472 SEQ:8
L:2167 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1469 Found:1472 SEQ:8
L:2369 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:2622 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:2878 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
M:332 Repeated in SeqNo=11
L:3137 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:3484 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
M:332 Repeated in SeqNo=14
L:3739 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:17
L:3753 M:254 E: No. of Bases conflict, LENGTH:Input:142 Counted:32 SEQ:18
L:3753 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:3753 M:252 E: No. of Seq. differs, <211> LENGTH:Input:31 Found:32 SEQ:18